

## RAW SEQUENCE LISTING

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Application Serial Number: 10/768,951  
Source: IFWO  
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IFWO

## RAW SEQUENCE LISTING

DATE: 03/18/2005

PATENT APPLICATION: US/10/768,951

TIME: 10:39:32

Input Set : A:\SEQLIST.txt

Output Set: N:\CRF4\03182005\J768951.raw

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3 <110> APPLICANT: COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH
5 <120> TITLE OF INVENTION: STABLE GENE VARIANTS OF LIPASES
7 <130> FILE REFERENCE: 71914
9 <140> CURRENT APPLICATION NUMBER: US 10/768,951
10 <141> CURRENT FILING DATE: 2004-01-29
12 <160> NUMBER OF SEQ ID NOS: 12
14 <170> SOFTWARE: PatentIn version 3.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 181
18 <212> TYPE: PRT
19 <213> ORGANISM: Bacillus subtilis
21 <220> FEATURE:
W--> 22 <221> NAME/KEY: AMINO ACIDS
23 <222> LOCATION: (1)..(181)
24 <223> OTHER INFORMATION: enzyme sequence
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29 Met Ala Glu His Asn Pro Val Val Met Val His Gly Ile Gly Gly Ala
30 1 5 10 15
33 Ser Phe Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp
34 20 25 30
37 Ser Arg Asp Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr
38 35 40 45
41 Asn Tyr Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu
42 50 55 60
45 Asp Glu Thr Gly Ala Lys Lys Val Asp Ile Val Ala His Ser Met Gly
46 65 70 75 80
49 Gly Ala Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys
50 85 90 95
53 Val Ala Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Gly
54 100 105 110
57 Lys Ala Leu Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser
58 115 120 125
61 Ile Tyr Ser Ser Ala Asp Met Ile Val Met Asn Tyr Leu Ser Arg Leu
62 130 135 140
65 Asp Gly Ala Arg Asn Val Gln Ile His Gly Gly His Ile Gly Leu Leu
66 145 150 155 160
69 Tyr Ser Ser Gln Val Asn Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly
70 165 170 175
73 Gly Gln Asn Thr Asn
74 180
77 <210> SEQ ID NO: 2
78 <211> LENGTH: 181
79 <212> TYPE: PRT

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80 <213> ORGANISM: Bacillus subtilis
82 <220> FEATURE:
W--> 83 <221> NAME/KEY: Amino acid
84 <222> LOCATION: (1)..(181)
85 <223> OTHER INFORMATION: Protein sequence
88 <400> SEQUENCE: 2
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91 1 5 10 15
94 Ser Phe Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp
95 20 25 30
98 Ser Arg Asp Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr
99 35 40 45
102 Asn Tyr Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu
103 50 55 60
106 Asp Glu Thr Gly Ala Lys Lys Val Asp Ile Val Ala His Ser Met Gly
107 65 70 75 80
110 Gly Ala Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys
111 85 90 95
114 Val Ala Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Gly
115 100 105 110
118 Lys Ala Leu Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser
119 115 120 125
122 Ile Tyr Ser Ser Ala Asp Met Ile Val Met Asn Tyr Leu Ser Arg Leu
123 130 135 140
126 Asp Gly Ala Arg Asn Val Gln Ile His Gly Gly His Ile Gly Leu Leu
127 145 150 155 160
130 Tyr Ser Ser Gln Val Tyr Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly
131 165 170 175
134 Gly Gln Asn Thr Asn
135 180
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143 <220> FEATURE:
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145 <222> LOCATION: (1)..(181)
146 <223> OTHER INFORMATION: Protein sequence
149 <400> SEQUENCE: 3
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152 1 5 10 15
155 Ser Phe Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp
156 20 25 30
159 Ser Arg Asp Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr
160 35 40 45
163 Asn Tyr Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu
164 50 55 60
167 Asp Glu Thr Gly Val Lys Lys Val Asp Ile Val Ala His Ser Met Gly
168 65 70 75 80

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171 Gly Ala Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys
172      85      90      95
175 Val Ala Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Gly
176      100     105     110
179 Lys Ala Leu Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser
180      115     120     125
183 Ile Tyr Ser Ser Asp Asp Met Ile Val Met Asn Tyr Leu Ser Arg Leu
184      130     135     140
187 Asp Gly Ala Arg Asn Val Gln Ile His Gly Gly His Ile Gly Leu Leu
188 145      150     155     160
191 Tyr Ser Ser Gln Val Tyr Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly
192      165     170     175
195 Gly Gln Asn Thr Asn
196      180

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199 &lt;210&gt; SEQ ID NO: 4

200 &lt;211&gt; LENGTH: 181

201 &lt;212&gt; TYPE: PRT

202 &lt;213&gt; ORGANISM: Bacillus subtilis

204 &lt;220&gt; FEATURE:

W--&gt; 205 &lt;221&gt; NAME/KEY: Amino acid

206 &lt;222&gt; LOCATION: (1)..(181)

207 &lt;223&gt; OTHER INFORMATION: Protein Sequence

210 &lt;400&gt; SEQUENCE: 4

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212 Met Ala Glu His Asn Pro Val Val Met Val His Gly Ile Gly Gly Ala
213 1      5      10      15
216 Ser Phe Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp
217      20      25      30
220 Ser Arg Asp Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr
221      35      40      45
224 Asn Tyr Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu
225      50      55      60
228 Asp Glu Thr Gly Thr Lys Lys Val Asp Ile Val Ala His Ser Met Gly
229 65      70      75      80
232 Gly Ala Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys
233      85      90      95
236 Val Ala Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Gly
237      100     105     110
240 Lys Ala Pro Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser
241      115     120     125
244 Ile Tyr Ser Ser Ala Asp Met Ile Val Met Asn Tyr Leu Ser Arg Leu
245      130     135     140
248 Asp Gly Ala Arg Asn Val Gln Ile His Gly Gly His Ile Gly Leu Leu
249 145      150     155     160
252 Tyr Ser Ser Gln Val Tyr Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly
253      165     170     175
256 Gly Gln Asn Thr Asn
257      180
260 <210> SEQ ID NO: 5
261 <211> LENGTH: 181

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262 <212> TYPE: PRT
263 <213> ORGANISM: Bacillus subtilis
265 <220> FEATURE:
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267 <222> LOCATION: (1)..(181)
268 <223> OTHER INFORMATION: Protein Sequence
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274 1 5 10 15
277 Ser Phe Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp
278 20 25 30
281 Ser Arg Asp Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr
282 35 40 45
285 Asn Tyr Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu
286 50 55 60
289 Asp Glu Thr Gly Ala Lys Lys Val Asp Ile Val Ala His Ser Met Gly
290 65 70 75 80
293 Gly Ala Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys
294 85 90 95
297 Val Ala Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Gly
298 100 105 110
301 Lys Ala Leu Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser
302 115 120 125
305 Ile Tyr Ser Ser Asp Asp Met Ile Val Met Asn Tyr Leu Ser Arg Leu
306 130 135 140
309 Asp Gly Ala Arg Asn Val Gln Ile His Gly Gly His Ile Gly Leu Leu
310 145 150 155 160
313 Tyr Ser Ser Gln Val Tyr Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly
314 165 170 175
317 Gly Gln Asn Thr Asn
318 180
321 <210> SEQ ID NO: 6
322 <211> LENGTH: 181
323 <212> TYPE: PRT
324 <213> ORGANISM: Bacillus subtilis
326 <220> FEATURE:
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328 <222> LOCATION: (1)..(181)
329 <223> OTHER INFORMATION: Protein sequence
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335 1 5 10 15
338 Ser Phe Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp
339 20 25 30
342 Ser Arg Asp Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr
343 35 40 45
346 Asn Tyr Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu
347 50 55 60
350 Asp Glu Thr Gly Ala Lys Lys Val Asp Ile Val Ala His Ser Met Gly

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351 65          70          75          80
354 Gly Ala Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys
355          85          90          95
358 Val Ala Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Gly
359          100          105          110
362 Lys Ala Pro Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser
363          115          120          125
366 Ile Tyr Ser Ser Asp Asp Met Ile Val Met Asn Tyr Leu Ser Arg Leu
367          130          135          140
370 Asp Gly Ala Arg Asn Val Gln Ile His Gly Gly His Ile Gly Leu Leu
371 145          150          155          160
374 Tyr Ser Ser Gln Val Tyr Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly
375          165          170          175
378 Gly Gln Asn Thr Asn
379          180
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383 <211> LENGTH: 181
384 <212> TYPE: PRT
385 <213> ORGANISM: Bacillus subtilis
387 <220> FEATURE:
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389 <222> LOCATION: (1)..(181)
390 <223> OTHER INFORMATION: Protein sequence
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395 Met Ala Glu His Asn Pro Val Val Met Val His Gly Ile Gly Gly Ala
396 1          5          10          15
399 Ser Phe Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp
400          20          25          30
403 Ser Arg Asp Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr
404          35          40          45
407 Asn Tyr Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu
408          50          55          60
411 Asp Glu Thr Gly Ala Lys Lys Val Asp Ile Val Ala His Ser Met Gly
412 65          70          75          80
415 Gly Ala Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys
416          85          90          95
419 Val Ala Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Gly
420          100          105          110
423 Lys Ala Leu Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser
424          115          120          125
427 Ile Tyr Ser Ser Ala Asp Met Ile Val Met Asn Tyr Leu Ser Arg Leu
428          130          135          140
431 Asp Gly Ala Ser Asn Val Gln Ile His Gly Gly His Ile Gly Leu Leu
432 145          150          155          160
435 Tyr Ser Ser Gln Val Tyr Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly
436          165          170          175
439 Gly Gln Asn Thr Asn
440          180
443 <210> SEQ ID NO: 8

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**VERIFICATION SUMMARY**

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TIME: 10:39:33

Input Set : A:\SEQLIST.txt

Output Set: N:\CRF4\03182005\J768951.raw

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L:144 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:205 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:266 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:327 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:388 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7  
L:449 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8  
L:510 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9  
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